U.S. Application No. 09/019,441

SEQUENCE LISTING

15

<120> GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS

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<140> 09/019,441
<141> 1998-02-05
<150> 08/803,085
<151> 1997-02-20
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                                     -10
tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct
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144

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Gly Gly Tyr 30	aac tat Asn Tyr												192	
ccc aaa ctc Pro Lys Leu		Tyr 2											240	
gat cgc ttc Asp Arg Phe													288	
tct ggg ctc Ser Gly Leu 80													336	
aca acc agt Thr Thr Ser 95		Leu											384	
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Leu Gly

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110 <210> 3 <211> 423 <212> DNA <213> Artifical Sequence <223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning <220> <221> misc feature <222> (1)..(57) <223> leader sequence <220> <221> mat_peptide <222> (58)..(423) <220> <221> CDS <222> (1)..(423) <400> 3 atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48 Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp -15 -10 96 gtc ctg tcc cag ctg cag ctg cag gag tcg ggc cca gga gtg gtg aag Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys _ 1 1 cet teg gag ace etg tee etc ace tge get gte tet gge tet gte 144 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val 15 20 age agt agt aac tgg tgg ace tgg ate ege cag eee eea ggg aag gga 192 Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly 30 35 ctq qaq tqq att qqa cqt atc tct qqt aqt qqt qqq gcc acc aac tac 240 Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr 50 60 aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag 288 Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys 65 70 75 aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala 80 gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu

100

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        -20
                            -15
ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc
                                                                   96
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
                     -1
ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
                 15
                                     20
cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa
Gln Asp İle Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc
                                                                   240
Ala Pro Lys Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
                             50
cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc
                                                                   288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
     60
gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag
                                                                   336
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
75
                     80
gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc
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Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

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-5
                     -1
                          1
                                          5
                                                              10
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
                                     20
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Ieu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
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gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag
                                                                   96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Ala Lys
cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
     15
                         20
                                             25
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Thr Phe Asn A	ac tac tac sn Tyr Tyr 35							192
ggg ctg gag to Gly Leu Glu T								240
tac gca gac to Tyr Ala Asp So								288
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gct gtc tat to Ala Val Tyr Ty 95								384
cag gga gtc c Gln Gly Val L 110								411
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